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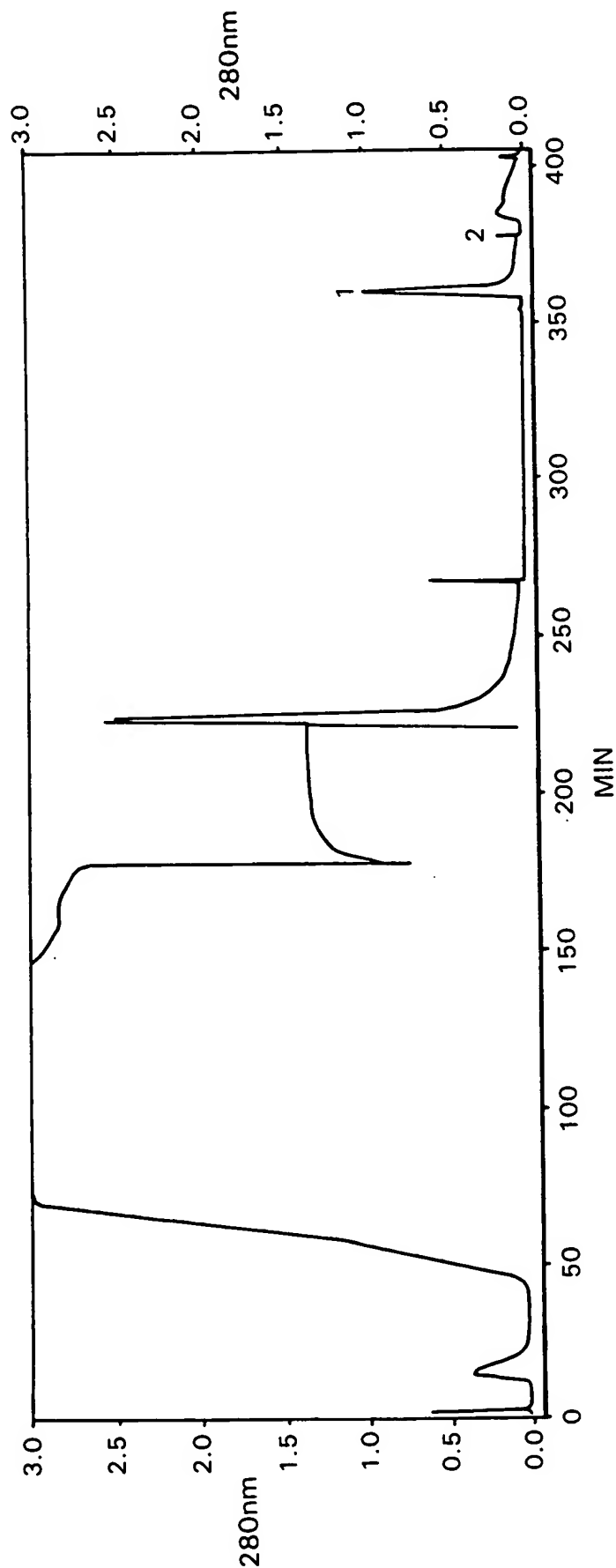
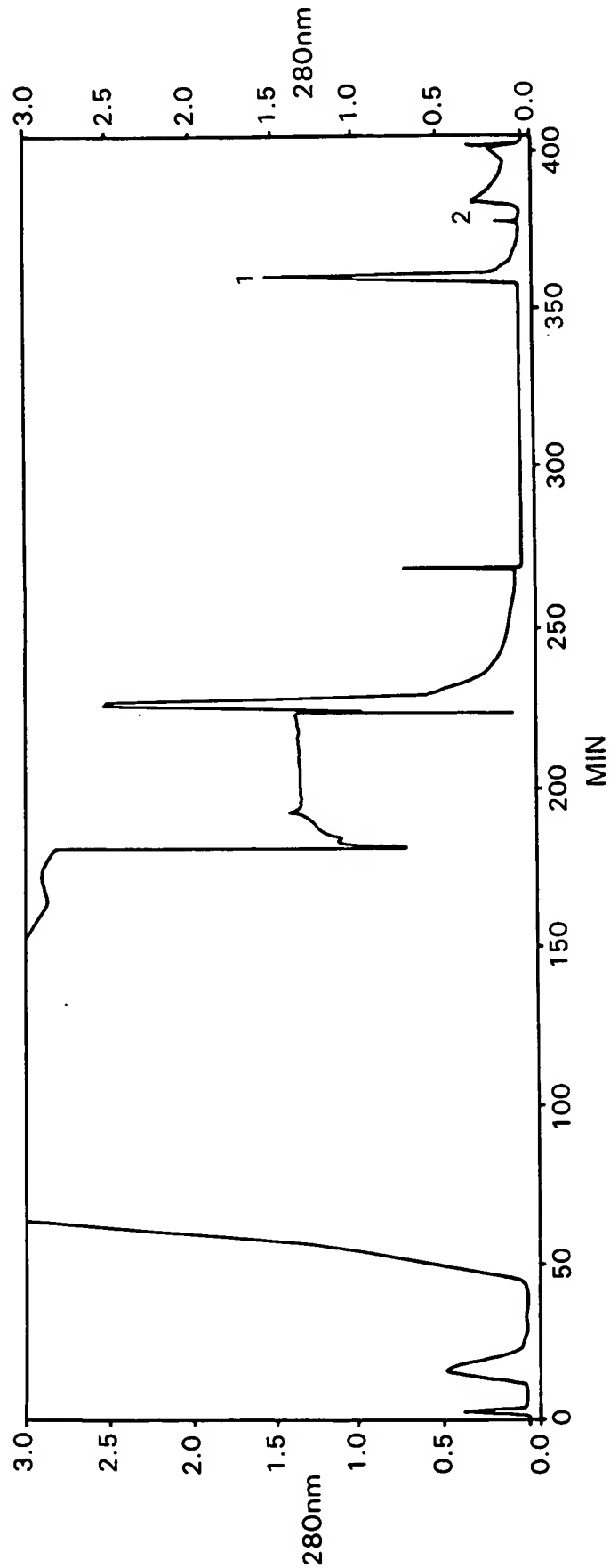
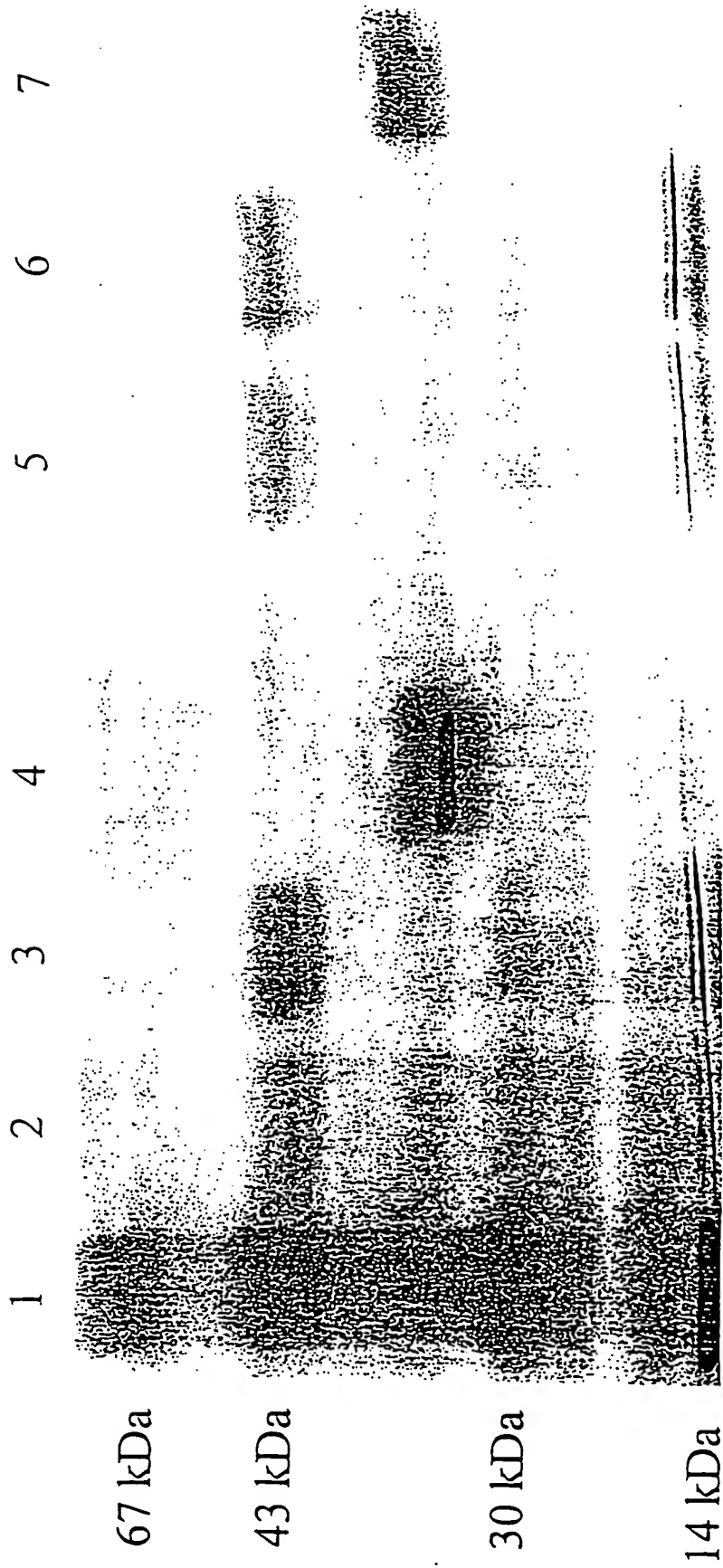


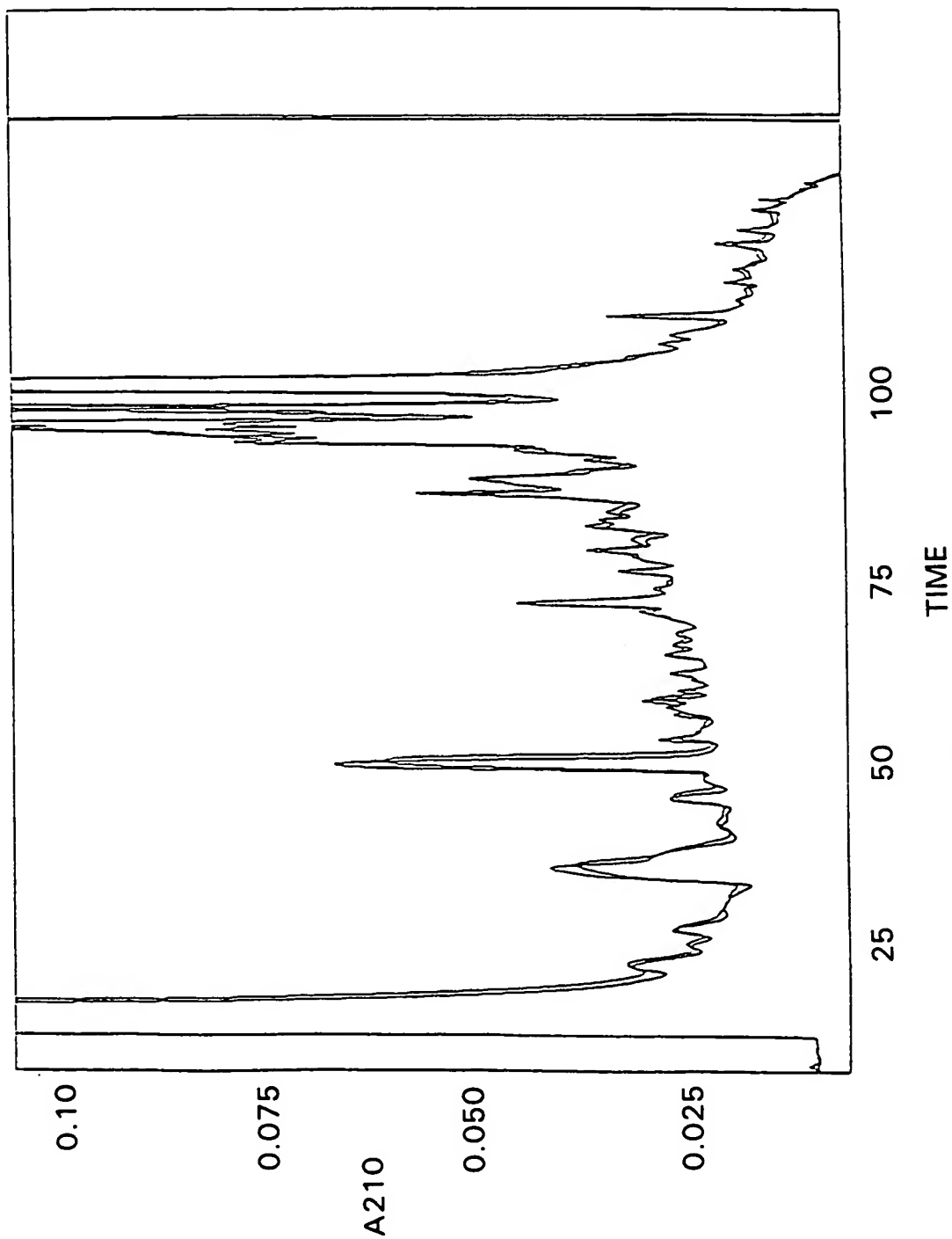
FIG. 1A



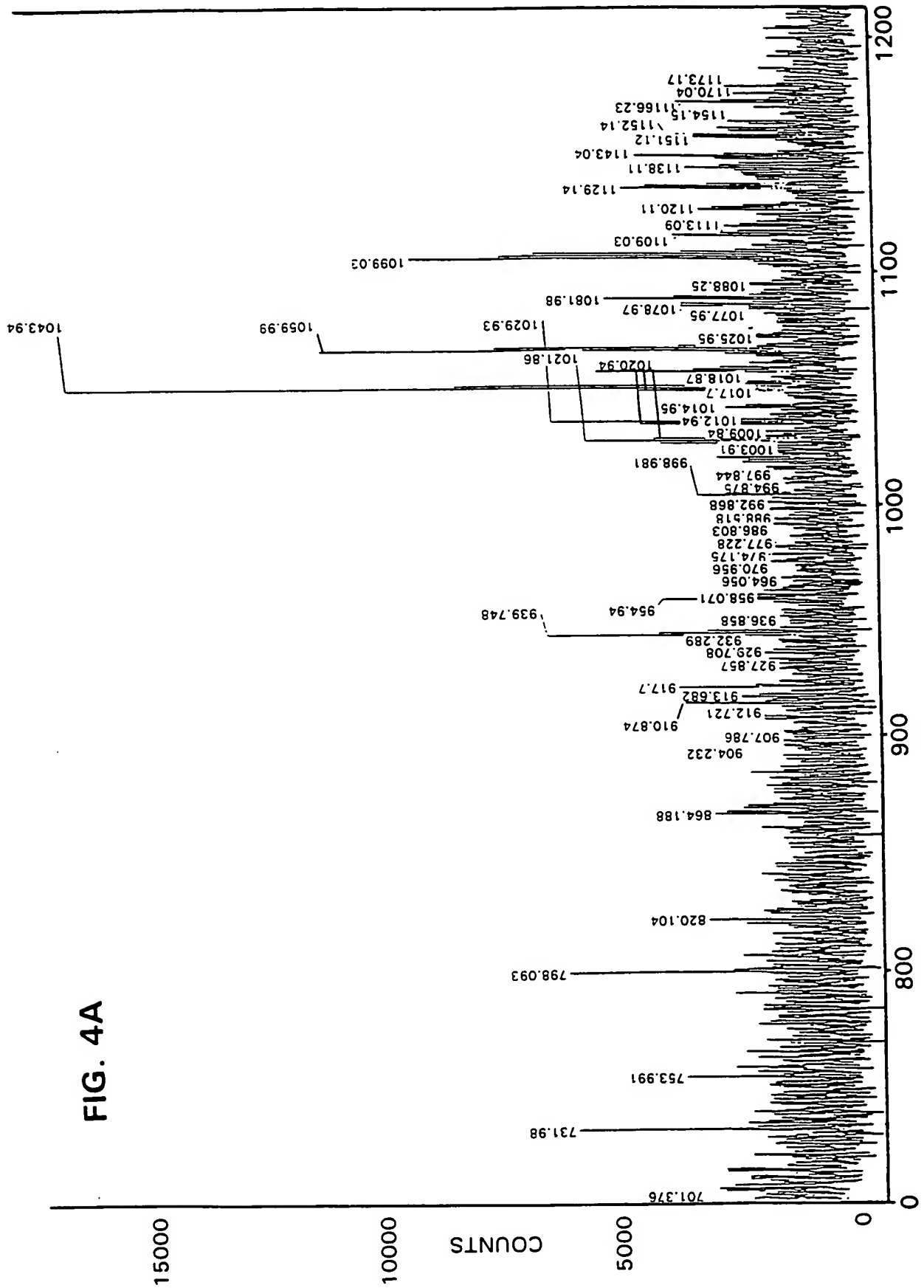
**FIG. 1B**

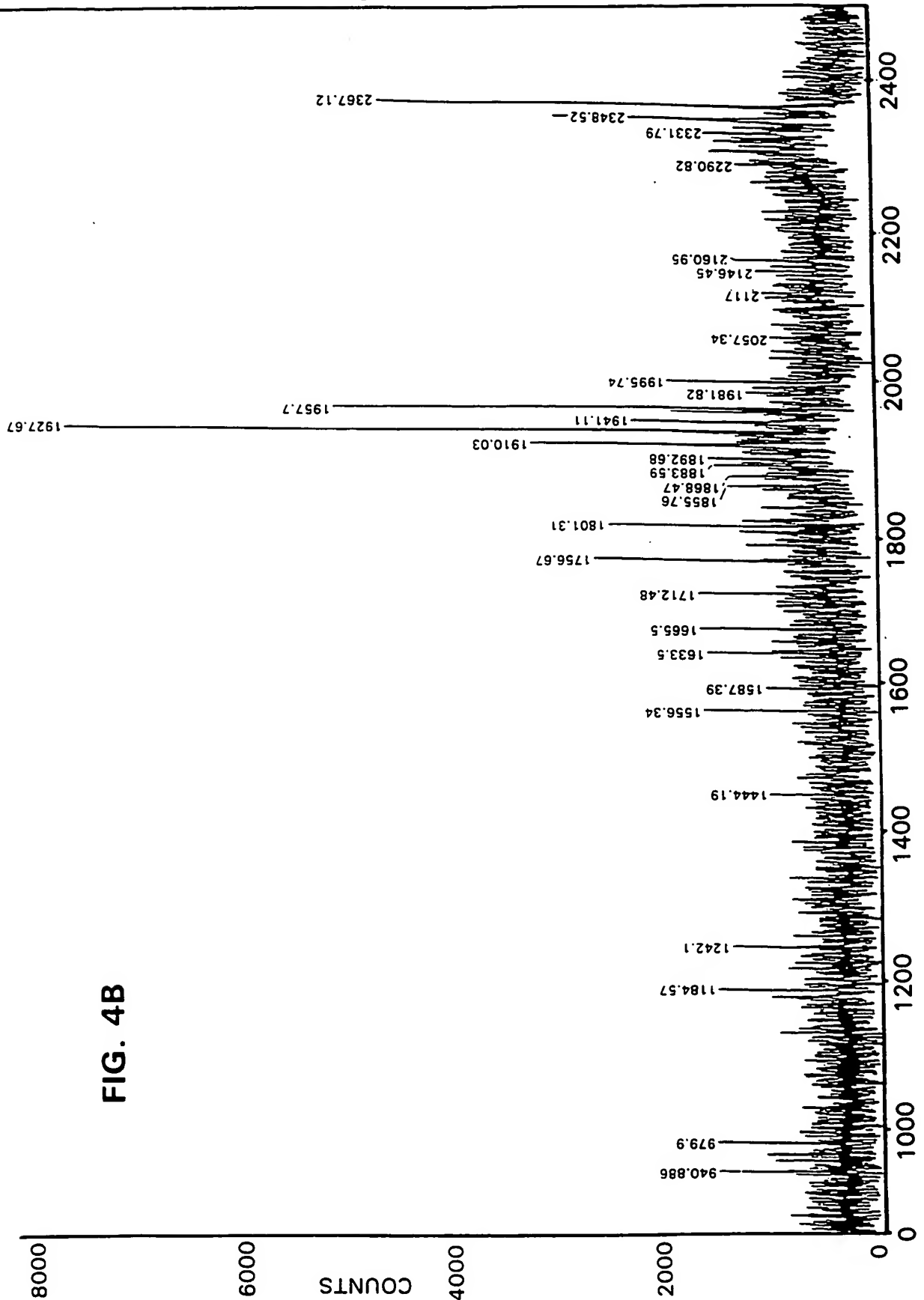


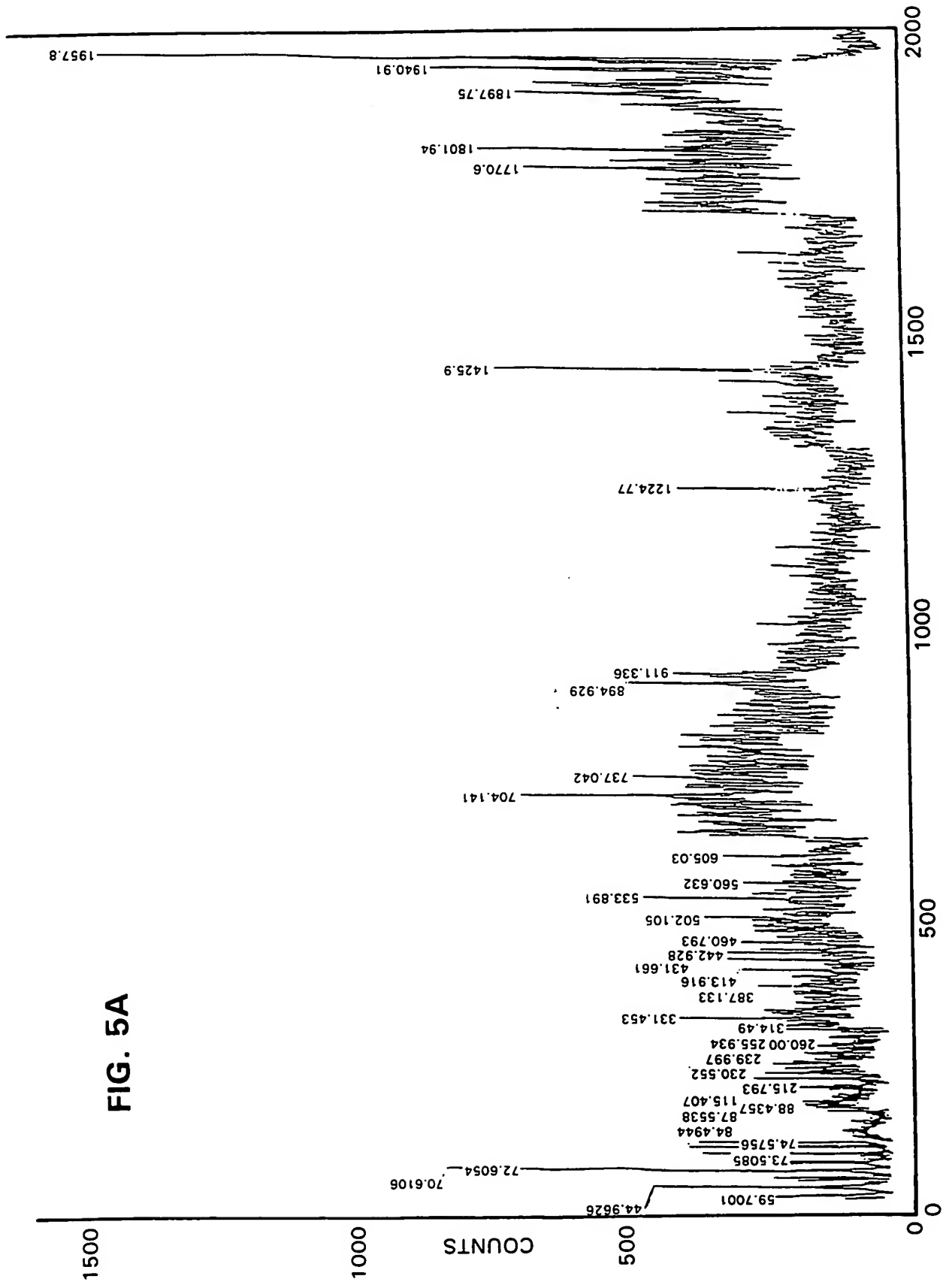
**FIG. 2**



**FIG. 3**







Sample ID (comment): R4A3F37m1957  
 Database searched: NCBIhr.7.5.97  
 Molecular weight search (1000-100000 Da) selects 269572 entries.  
 Species search (HOMO SAPIENS) selects 22771 entries.  
 Combined molecular weight and species searches select 20933 entries.  
 Number of sequences passing through parent mass filter: 84015  
 Ion Types Considered: a b y n h i  
 search selects 257 entries

Result Summary									
Search Mode Identity	Max. # Unmatched Ions	Peptide Masses are Par(ml)Frag(av)	Digest Used No enzyme	Max. # Missed Cleavages	Cysteines Modified by unmodified	Peptide N terminus Hydrogen (H)	Peptide C terminus Free Acid (O H)	# Unmatched Ions	Protein Name
Parent mass. 1957.2000 (+/-500.0000ppm) Fragment Ions present: (RPV)(NR)(IKQ)FSDR									
Rank	MS-Digest Index#	NCBIhr.7.597 Accession#	Protein MW (Da)	Species	Calculated MH+ (Da)	MH+ Error (Da)	Sequence	# Unmatched Ions	Protein Name
1	240839	1819795	21251.4	HOMO SAPIENS	1956.9052	0.2948	(Y)VDDTQFVRFSDDAASQR(M)	2	(D82930) HLA-A26-variant
1	152874	915219	40679.8	HOMO SAPIENS	1956.9052	0.2948	(Y)VDDTQFVRFSDDAASQR(M)	2	(U25971) MHC class 1 antigen HLA-A2407
1	141923	825673	20921.2	HOMO SAPIENS	1956.9052	0.2948	(Y)VDDTQFVRFSDDAASQR(M)	2	(X82161) HLA-A alpha1 and alpha2 domains
1	159176	994765	41113.1	HOMO SAPIENS	1956.9052	0.2948	(Y)VDDTQFVRFSDDAASQR(M)	2	(D32129) HLA-A26
1	282322	250934	38703.4	HOMO SAPIENS	1956.9052	0.2948	(Y)VDDTQFVRFSDDAASQR(M)	2	(Z97370) human leukocyte antigen
1	133479	717123	40895.1	HOMO SAPIENS	1956.9052	0.2948	(Y)VDDTQFVRFSDDAASQR(M)	2	(U18930)MHC class 1 antigen HLA-A2
1	49436	785055	38355.8	HOMO SAPIENS	1956.9052	0.2948	(Y)VDDTQFVRFSDDAASQR(M)	2	(M160010) HLA-AH class 1 antigen (AA at 30)
1	277806	2394324	10423.4	HOMO SAPIENS	1956.9052	0.2948	(Y)VDDTQFVRFSDDAASQR(M)	2	(AF017310) MHC class 1 antigen
1	277805	2394322	10430.3	HOMO SAPIENS	1956.9052	0.2948	(Y)VDDTQFVRFSDDAASQR(M)	2	(AF017309) MHC class 1 antigen
1	277713	2394009	21027.3	HOMO SAPIENS	1956.9052	0.2948	(Y)VDDTQFVRFSDDAASQR(M)	2	(AF012767) MHC class 1 antigen HLA-A heavy chain

FIG. 5B



gb/AA548636/AA548636.nj.38402.s1.NCI.CGAP.AA1.Homo.Sapiens.cDNA.clone  
IMAGE.994755.similar.to.gb:z46633.HLA.CLASS.I.HISTOCOMPATIBILITY  
ANTIGEN,A-2.A\*0201.ALPHA.(HUMAN);  
Length = 539

Plus Strand HSPs:

Score = 30 (41.9 bits), Expect = 8.1e-05, P = 8.1e-05  
Identities = 18/18 (100%), Positives = 18/18 (100%), Frame = +2

Query: 1 VDDTQFVRFDSDAASQRM 18  
VDDTQFVRFDSDAASQRM  
Sbjct: 152 VDDTQFVRFDSDAASQRM 205

gb/AA147151/AA147151.zo32d06.r1.Stratagene.colon.(#937204).Homo.sapiens  
cDNA.clone.5885875.similar.to.gb:M64740.HLA.CLASS.I  
HISTOCOMPATIBILITY.ANTIGEN,A-24.(A-9).A\*2402.ALPHA.(HUMAN);  
Length = 581

Plus Strands HSPs:

Score = 90 (41.9 bits), Expect = 8.1e-05, P = 8.1e-05  
Identities = 18/18 (100%), Positives = 18/18 (100%), Frame = +1

Query: 1 VDDTQFVRFDSDAASQRM 18  
VDDTQFVRFDSDAASQRM  
Sbjct: 13 VDDTQFVRFDSDAASQRM 66

gb/H23377/H23377.ym57e02.r1.Homo.sapiens.cDNA.clone.52227.5'.similar.to  
gb:x00492.cdsl.HLA.CLASS.I.HISTOCOMPATIBILITY.ANTIGEN,A-3A.A\*0301  
ALPHA.(HUMAN);  
Length = 459

Plus Strand HSPs:

Score = 90 (41.9 bits), Expect = 8.1e-05, P = 8.1e-05  
Identities = 18/18 (100%), Positives = 18/18 (100%), Frame = +1

Query: 1 VDDTQFVRFDSDAASQRM 18  
VDDTQFVRFDSDAASQRM  
Sbjct: 154 VDDTQFVRFDSDAASQRM 207

gb/RI13904/RI13904.yf62c03.r1.Homo.sapiens.cDNA.clone.26801.5'.similar.to  
gb:m64742.cdsl.HLA.CLASS.I.HISTOCOMPATIBILITY.ANTIGEN,A-23(A-9)  
A\*2301.(HUMAN);  
Length = 459

Plus Strand HSPs:

Score = 90 (41.9 bits), Expect = 8.1e-05, P = 8.1e-05  
Identities = 18/18 (100%), Positives = 18/18 (100%), Frame = +2

Query: 1 VDDTQFVRFDSDAASQRM 18  
VDDTQFVRFDSDAASQRM  
Sbjct: 146 VDDTQFVRFDSDAASQRM 199

gb/RI12066/RI12066.yf54d10.r1.Homo.sapiens.cDNA.clone.26062.5'.similar.to  
gb:x00492.cdsl.HLA.CLASS.I.HISTOCOMPATIBILITY.ANTIGEN,A-3A\*0301  
alpha.(human);  
Length = 405

Plus Strand HSPs:

Score = 90 (41.9 bits), Expect = 8.1e-05, P = 8.1e-05  
Identities = 18/18 (100%), Positives = 18/18 (100%), Frame = +2

Query: 1 VDDTQFVRFDSDAASQRM 18  
VDDTQFVRFDSDAASQRM  
Sbjct: 158 VDDTQFVRFDSDAASQRM 211

gb/AA132653/AA132653.zo21a05.r1.Stratagene.colon.(#937204).Homo.sapiens  
cDNA.clone.587504.5'.similar.to.gb:z46633.HLA.CLASS.I  
HISTOCOMPATIBILITY.ANTIGEN,A-2.A\*0201.ALPHA.(HUMAN);  
Length = 428

Plus Strand HSPs:

Score = 90 (41.9 bits), Expect = 8.1e-05, P = 8.1e-05  
Identities = 18/18 (100%), Positives = 18/18 (100%), Frame = +3

Query: 1 VDDTQFVRFDSDAASQRM 18  
VDDTQFVRFDSDAASQRM  
Sbjct: 158 VDDTQFVRFDSDAASQRM 203

gb/R59764/R59764.yh07c05.r1.Homo.sapiens.cDNA.clone.42563.5'.similar.to  
gb:x00492.cdsl.HLA.CLASS.I.HISTOCOMPATIBILITY.ANTIGEN,A-3.A\*0301  
ALPHA.(HUMAN);  
Length = 461

Plus Strands HSPs:

Score = 90 (41.9 bits), Expect = 8.1e-05, P = 8.1e-05  
Identities = 18/18 (100%), Positives = 18/18 (100%), Frame = +1

Query: 1 VDDTQFVRFDSDAASQRM 18  
VDDTQFVRFDSDAASQRM  
Sbjct: 138 VDDTQFVRFDSDAASQRM 210

gb/AA488534/AA488534.ab37f08.r1.Stratagene.HeLa.cell.s3.937216.Homo  
sapiens.cDNA.clone.843015.5'.similar.to.gb:L06425.HLA.CLASS.I  
HISTOCOMPATIBILITY.ANTIGEN,AW-34(A-10).A\*3402.ALPHA.(HUMAN);  
Length = 478

Plus Strand HSPs:

Score = 90 (41.9 bits), Expect = 8.1e-05, P = 8.1e-05  
Identities = 18/18 (100%), Positives = 18/18 (100%), Frame = +3

Query: 1 VDDTQFVRFDSDAASQRM 18  
VDDTQFVRFDSDAASQRM  
Sbjct: 138 VDDTQFVRFDSDAASQRM 191

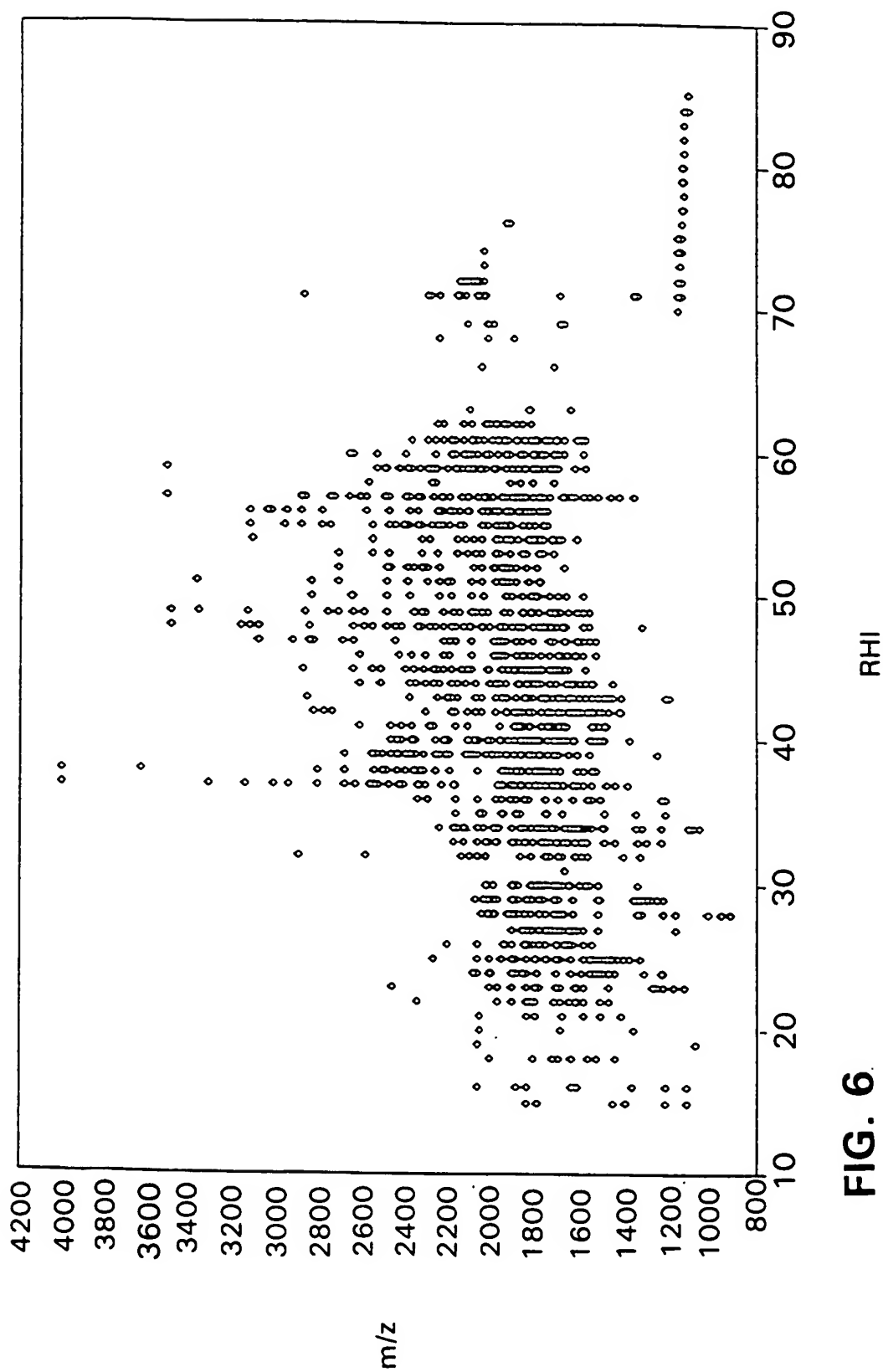


FIG. 6

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